GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:06:55 ; Search time 755.06 Seconds
(without alignments)
28.386 Million cell updates/sec

Title: US-09-851-670-4
Perfect score: 25
Sequence: 1 acagtagcagcaacagcatgagacc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17.6	70.4	38	20	AAZ06984	Murine GABA B rece
c 2	17.6	70.4	38	22	AAC91918	Murine GABA-B-R1a
c 3	17.6	70.4	54	21	AAA73946	GFP Leu(CTG)5 forw
c 4	16.6	66.4	29	21	AAA04264	Polymorphic fragme
c 5	16.6	66.4	48	19	AAV68375	Clone #1 fragment
6	16.2	64.8	36	18	AAT78910	Poly-glutamine rep
7	16.2	64.8	54	18	AAT78909	Poly-glutamine rep
8	16.2	64.8	57	19	AAV17235	SCA2 gene CAG repe
c 9	16	64.0	45	22	AAH24422	Oligonucleotide en
c 10	16	64.0	54	22	AAH24423	Oligonucleotide en
11	15.8	63.2	20	21	AAA66287	Dog genomic marker
c 12	15.8	63.2	29	21	AAA04482	Polymorphic fragme
c 13	15.8	63.2	38	22	AAH48359	Human FOAP-9 PCR p
c 14	15.8	63.2	40	22	AAC87437	Human SEAP alkalin
c 15	15.8	63.2	40	22	AAC87489	Human SEAP alkalin
c 16	15.8	63.2	41	20	AAX58073	PCR primer for hum
c 17	15.8	63.2	41	21	AAZ29439	PCR primer JC139 f
c 18	15.8	63.2	50	20	AAX58113	PCR primer for hum
c 19	15.8	63.2	50	20	AAX58091	PCR primer for can
c 20	15.8	63.2	50	20	AAX58075	PCR primer for hum
c 21	15.8	63.2	52	20	AAX26920	Sense PCR primer u
c 22	15.8	63.2	52	20	AAX19670	Human SEAP gene PC
c 23	15.8	63.2	52	21	AAA54362	Primer for amplify
c 24	15.8	63.2	52	21	AAA99543	SEAP reporter plas
c 25	15.8	63.2	52	21	AAA99562	SEAP reporter plas
c 26	15.8	63.2	52	21	AAA99581	SEAP reporter plas
c 27	15.8	63.2	52	21	AAA99600	SEAP reporter plas
c 28	15.8	63.2	52	21	AAA94417	Sense strand N-ter
c 29	15.8	63.2	52	21	AAA63351	Human secreted alk
c 30	15.8	63.2	52	21	AAA64979	Human secreted alk
c 31	15.8	63.2	52	21	AAA53530	Secreted alkaline
c 32	15.8	63.2	52	21	AAA28741	Sense primer for N
c 33	15.8	63.2	52	21	AAA13693	Human SEAP gene PC
c 34	15.8	63.2	52	21	AAA13774	Human SEAP gene PC
c 35	15.8	63.2	52	21	AAZ60492	PCR primer used to
c 36	15.8	63.2	52	21	AAZ58847	Human SEAP gene am
c 37	15.8	63.2	52	21	AAZ35452	SEAP N-terminal re
c 38	15.8	63.2	52	21	AAZ35471	SEAP N-terminal re
c 39	15.8	63.2	52	22	AAF87068	PCR primer 1 used
c 40	15.8	63.2	52	22	AAF82121	Human SEAP gene se
c 41	15.8	63.2	52	22	AAF77222	Human SEAP cDNA sp
c 42	15.8	63.2	52	22	AAF59698	Human SEAP PCR pri
c 43	15.8	63.2	52	22	AAF57890	Human SEAP PCR pri
c 44	15.8	63.2	52	22	AAF23751	Human SEAP PCR pri
c 45	15.6	62.4	24	20	AAX60748	Heat shock protein

ALIGNMENTS

RESULT 1
AAZ06984/c
ID AAZ06984 standard; DNA; 38 BP.
XX
AC AAZ06984;
XX
DT 15-NOV-1999 (first entry)
XX
DE Murine GABA B receptor subunit GABABR1a PCR primer 472408 sense.
XX
KW Gamma-amino-butyric acid B receptor subunit; HG20; GABABR1a;
KW depression; epilepsy; neuropsychiatric disorder; dementia;
KW muscular contraction; central nervous system disorder; PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9940114-A1.
XX
PD 12-AUG-1999.
XX
PF 03-FEB-1999; 99WO-US02361.
XX
PR 05-FEB-1998; 98US-0073767.
XX
PA (MERI) MERCK & CO INC.
PA (MERI) MERCK FROSST CANADA INC.
PA (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.
PA (USSH) US NAT INST OF HEALTH.
XX
PI Bonner TI, Bonnert TP, Clark J, Kolakowski LF, Liu Q;
PI McDonald T, Ng GYK;
XX
DR WPI; 1999-527300/44.

XX
PT New DNA encoding human and murine receptor subunits, useful for
PT identifying agonists and antagonists for treatment of depression,
PT epilepsy and neuropsychiatric disorders
XX
PS Example 6; Page 72; 128pp; English.
XX
CC The present invention describes two gamma-amino-butyric acid (GABA)
CC B receptor (GABABR) subunits designated HG20 and GABABR1a. Cells
CC expressing the new receptor subunits are useful for identifying GABABR
CC agonists and antagonists. HG20 proteins and their antagonists are useful
CC for inhibiting HG20 or GABABR function, useful for treating depression,
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
CC and central nervous system disorders. The present sequence represents
CC a PCR primer for murine GABABR1a, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 38 BP; 4 A; 11 C; 12 G; 11 T; 0 other;

Query Match 70.4%; Score 17.6; DB 20; Length 38;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgagacc 25
||| ||||||| ||||||| |||
Db 32 CAGCAGCAGCAGCAGCATGGTACC 9

RESULT 2
AAC91918/c
ID AAC91918 standard; DNA; 38 BP.
XX
AC AAC91918;
XX
DT 19-MAR-2001 (first entry)
XX
DE Murine GABA-B-R1a probe #1.
XX
KW Murine; gamma-amino-butyric acid receptor; GABA-B; probe; ss.
XX
OS Mus sp.
XX
PN WO200073788-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-CA00638.
XX
PR 01-JUN-1999; 99US-0137025.
XX
PA (MERI) MERCK FROSST CANADA & CO.
XX
PI Ng G, O'Neil G;
XX
DR WPI; 2001-049959/06.
XX
PT Use of gabapentin, 1-(aminomethyl)cyclohexaneacetic acid, in assays for
PT identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists
PT -
XX
PS Example 2; Page 41; 85pp; English.
XX
CC The present invention relates to a method for determining whether a
CC substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a
CC potential agonist or antagonist of the GABA-B receptor. The method
CC comprises exposing cells to 1-(aminomethyl)cyclohexaneacetic acid
CC (gabapentin) in the presence or absence of the substance under
CC investigation. The present sequence is a probe for murine GABA-B-R1a,
CC which was used in the present invention to construct a functional GABA-B
CC receptor, for use in the method of the present invention.
XX
SQ Sequence 38 BP; 4 A; 11 C; 12 G; 11 T; 0 other;

Query Match 70.4%; Score 17.6; DB 22; Length 38;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgagacc 25
||| ||||||| ||||||| |||
Db 32 CAGCAGCAGCAGCAGCATGGTACC 9

RESULT 3
AAA73946/c
ID AAA73946 standard; DNA; 54 BP.
XX
AC AAA73946;
XX
DT 06-DEC-2000 (first entry)
XX
DE GFP Leu(CTG)5 forward primer.
XX
KW Green fluorescent protein; GFP; reporter gene; codon utilisation;
KW translational efficiency; protein abundance; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200042215-A1.
XX
PD 20-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-AU00008.
XX
PR 08-JAN-1999; 99AU-0008078.
XX
PA (UYQU) UNIV QUEENSLAND.
PA (SUNX/) SUN X.
XX
PI Zhou J, Frazer IH;
XX
DR WPI; 2000-499118/44.
XX
PT Determining translational efficiency of codons in cells, comprising
PT introducing synthetic constructs with reporter genes fused in frame to
PT tandem repeats of the codon, and measuring expression -
XX
PS Example 1; Page 183; 190pp; English.
XX
CC The present sequence is a primer used to generate a synthetic gfp gene by
CC PCR amplification of a humanised gfp gene. A single artificial start
CC codon followed by a stretch of five identical codons was fused in frame
CC immediately upstream of a gfp coding sequence to form the synthetic gene.
CC The amplified fragment was cloned into the mammalian expression vector
CC pCDNA3, which contains SV40 ori and the CMV promoter, and was used in a
CC method for determining the translational efficiency of a codon in a cell.
CC The synthetic construct was introduced into COS-1 cells and expression of
CC the reporter protein (green fluorescent protein) was measured. A series
CC of 64 gfp reporter constructs was made in which the gfp gene is preceded
CC in frame by a tandem repeat of 5 identical codons. The series covers the
CC entire set of isoaccepting codon triplets. Codons with a higher
CC translational efficiency than their corresponding synonymous codons can
CC be identified. These codons may then be used to replace the less
CC preferred codons of a polynucleotide so that there is higher protein
CC expression within undifferentiated epithelial cells such as COS-1 cells.
XX
SQ Sequence 54 BP; 9 A; 14 C; 20 G; 11 T; 0 other;

Query Match 70.4%; Score 17.6; DB 21; Length 54;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgagacc 25
||| ||||||| ||||||| |||

```
Db      27 CAGCAGCAGCAGCAGCATGGTACC 4


RESULT   4
AAA04264/c
ID   AAA04264 standard; DNA; 29 BP.
XX
AC   AAA04264;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Polymorphic fragment of hypertension associated gene GGR.
XX
KW   Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW   Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW   Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
KW   polycystic kidney disease; von Willebrands disease; forensic; human;
KW   tuberous sclerosis; hereditary hemorrhagica telangiectasia;
KW   familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW   Ehlers-Danlos syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   EP955382-A2.
XX
PD   10-NOV-1999.
XX
PF   07-MAY-1999;   99EP-0250150.
XX
PR   07-MAY-1998;   98US-0084641.
PR   03-MAY-1999;   99US-0304232.
XX
PA   (AFFY-) AFFYMETRIX INC.
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   Fan JB,  Chakravarti A,  Haluska MR;
XX
DR   WPI; 2000-107928/10.
XX
PT   Novel nucleic acids containing polymorphisms used in the diagnosis of
PT   hypertension -
XX
PS   Claim 1; Page 31; 53pp; English.
XX
CC   The invention provides polymorphic fragments of genes associated with
CC   hypertension. The nucleic acids including the polymorphic sites can be
CC   used as probes or primers for expressing variant proteins. Detection of
CC   the polymorphisms is useful in designing prophylactic and therapeutic
CC   regimes customized to underlying abnormalities. The polymorphisms can be
CC   used for association studies for hypertension, and in hypertension
CC   diagnostic assays. Where the polymorphisms have strong correlation with
CC   hypertension, within a gene, they are likely to have a causative role in
CC   hypertension. This information can be used to find the precise role of a
CC   polymorphism in the disease, and this can be used to identify potential
CC   drugs which combat the disease. The polymorphisms can be tested for
CC   association with other diseases e.g. agammaglobulinemia, diabetes
CC   insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC   syndrome, Fabrys disease, familial hypercholesterolemia, polycystic
CC   kidney disease, hereditary spherocytosis, von Willebrands disease,
CC   tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC   colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC   acute intermittent porphyria. The polymorphic forms can also be used in
CC   forensics to identify individuals.
XX
SQ   Sequence 29 BP; 1 A; 10 C; 8 G; 9 T; 1 other;


  Query Match             66.4%;  Score 16.6;  DB 21;  Length 29;
  Best Local Similarity   94.1%;  Pred. No. 5e+02;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 cagtagcagcaacagca 18
           |||:|||||||||||||
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```
Db      18 CAGYAGCAGCAACAGCA 2


RESULT   5
AAV68375/c
ID   AAV68375 standard; DNA; 48 BP.
XX
AC   AAV68375;
XX
DT   10-MAR-1999  (first entry)
XX
DE   Clone #1 fragment identified by CAG repeat analysis method.
XX
KW   CAG repeat; human; genome analysis; medical diagnostic;
KW   nucleic acid analysis; variation assessment; neurological disease;
KW   Huntington's chorea; PCR suppression; ss.
XX
OS   Homo sapiens.
XX
PN   WO9849345-A1.
XX
PD   05-NOV-1998.
XX
PF   29-APR-1998;   98WO-US08616.
XX
PR   29-APR-1997;   97US-0045078.
XX
PA   (UYBO-) UNIV BOSTON.
XX
PI   Smith CL;
XX
DR   WPI; 1998-594983/50.
XX
PT   Analysing nucleic acid samples - using amplification primers which
PT   contain CAG or CTG tri:nucleotide repeats for differential display
PT   of samples from different sources
XX
PS   Example; Page 32; 44pp; English.
XX
CC   This sequence represents a fragment of a human CAG repeat containing
CC   clone DNA sequence isolated using the method of the invention. The method
CC   is for analysing nucleic acids in a sample, and comprises: (a) providing
CC   a sample containing nucleic acid, a first oligonucleotide primer
CC   comprising a CTG repeat, a second oligonucleotide primer comprising a
CC   CAG repeat and a polymerase and PCR reagents; (b) preparing the nucleic
CC   acid so that it is amplifiable; (c) amplifying the nucleic acid with the
CC   first and second primers; and (d) detecting the amplified product. The
CC   method is used to distinguish between the expression of genes in two or
CC   more biological samples, e.g. body fluids, cells, solid tissue or solid
CC   and liquid foods. It can be used in medical diagnostics, e.g. to
CC   differentiate between normal and diseased tissue or to assess the
CC   variation within monozygotic twin pairs. The method allows the isolation
CC   and analysis of genome subsets containing CAG repeats which are known to
CC   be important in a number of neurological diseases including Huntington's
CC   chorea. The method uses PCR suppression, in which only fragments which
CC   contain a target repeat are efficiently amplified. This allows accurate
CC   identification of differentially expressed genes in various cell types.
CC   Genome complexity is reduced by the new method which targets genomic
CC   subsets containing CAG repeats.
XX
SQ   Sequence 48 BP; 10 A; 13 C; 12 G; 13 T; 0 other;


  Query Match             66.4%;  Score 16.6;  DB 19;  Length 48;
  Best Local Similarity   82.6%;  Pred. No. 5.3e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 acagtagcagcaacagcatgaga 23
           |||| ||||||| |||||  |||
Db      24 ACAGCAGCAGCAGCAGCAGA 2


RESULT   6
```

AAT78910
ID AAT78910 standard; cDNA; 36 BP.
XX
AC AAT78910;
XX
DT 09-FEB-1998 (first entry)
XX
DE Poly-glutamine repeat region coding sequence from clone DAN26.
XX
KW Monoclonal antibody; neurodegenerative disease; polyglutamine; TBP;
KW repeat region; affinity; TATA binding protein; Kennedy disease;
KW transcription initiation factor; lymphoblastic cell line; schizophrenia;
KW Huntington's disease; dominant autosomal spinocerebellar ataxia;
KW X-linked spino-bulbular muscular atrophy; familial spastic paraplegia;
KW dentarorubral-pallidolusial atrophy; bipolar affective disorder;
KW manic depressive psychosis; ss.
XX
OS Homo sapiens.
XX
PN WO9717445-A1.
XX
PD 15-MAY-1997.
XX
PF 08-NOV-1996; 96WO-FR01773.
XX
PR 10-NOV-1995; 95FR-0013576.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Lutz Y, Mandel J, Tora L, Trottier Y;
XX
DR WPI; 1997-281034/25.
XX
PT Antibody 1C2 used for treating or preventing neuro-degenerative
PT diseases - associated with proteins containing long poly:glutam
PT repeats, e.g. Huntington's disease
XX
PS Claim 21; Page 44; 69pp; French.
XX
CC The invention relates to a monoclonal antibody (MAb) 1C2 for the
CC treatment of neurodegenerative diseases associated with the presence
CC of polyglutamine repeat regions. This MAb is already known for its
CC affinity to the TATA binding protein (TBP) transcription initiation
CC factor, especially at the amino acid sequence LEEQQRQQQQQQ found at
CC the N-terminus of TBP. MAb 1C2 has been shown to have a high affinity
CC for polyglutamine repeats with a proportional affinity to the number
CC of glutamine repeats. This affinity has been used to identify genes
CC encoding proteins containing long polyglutamine repeats which are
CC implicated in neurodegenerative diseases. A screen of an expression
CC library, generated from a lymphoblastic cell line from a patient
CC suffering from spinocerebellar ataxia (SCA), with MAb 1C2 isolated 6 new
CC sequences (AAT78906-T78911) encoding polyglutamine repeats. This
CC sequence is derived from clone DAN26 isolated from a patient suffering
CC from dominant autosomal SCA type 7. MAb 1C2, active fragment of it or
CC nucleic acids encoding it are specifically used to treat Huntington's
CC disease, SCA types 1-5 or 7, X-linked spino-bulbular muscular atrophy
CC (Kennedy disease), dentarorubral-pallidolusial atrophy, dominant
CC autosomal spinocerebellar ataxia, familial spastic paraplegia, bipolar
CC affective disorder, manic depressive psychoses and schizophrenia.
XX
SQ Sequence 36 BP; 13 A; 12 C; 11 G; 0 U; 0 other;

Query Match 64.8%; Score 16.2; DB 18; Length 36;
Best Local Similarity 85.7%; Pred. No. 7.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgag 22
||| |||||||||||| ||
Db 10 cagcagcagcaacagcagcag 30

RESULT 7
AAT78909
ID AAT78909 standard; cDNA; 54 BP.
XX
AC AAT78909;
XX
DT 09-FEB-1998 (first entry)
XX
DE Poly-glutamine repeat region coding sequence from clone DAN15.
XX
KW Monoclonal antibody; neurodegenerative disease; polyglutamine; TBP;
KW repeat region; affinity; TATA binding protein; Kennedy disease;
KW transcription initiation factor; lymphoblastic cell line; schizophrenia;
KW Huntington's disease; dominant autosomal spinocerebellar ataxia;
KW X-linked spino-bulbular muscular atrophy; familial spastic paraplegia;
KW dentarorubral-pallidolusial atrophy; bipolar affective disorder;
KW manic depressive psychosis; ss.
XX
OS Homo sapiens.
XX
PN WO9717445-A1.
XX
PD 15-MAY-1997.
XX
PF 08-NOV-1996; 96WO-FR01773.
XX
PR 10-NOV-1995; 95FR-0013576.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Lutz Y, Mandel J, Tora L, Trottier Y;
XX
DR WPI; 1997-281034/25.
XX
PT Antibody 1C2 used for treating or preventing neuro-degenerative
PT diseases - associated with proteins containing long poly:glutamine
PT repeats, e.g. Huntington's disease
XX
PS Claim 21; Page 44; 69pp; French.
XX
CC The invention relates to a monoclonal antibody (MAb) 1C2 for the
CC treatment of neurodegenerative diseases associated with the presence
CC of polyglutamine repeat regions. This MAb is already known for its
CC affinity to the TATA binding protein (TBP) transcription initiation
CC factor, especially at the amino acid sequence LEEQQRQQQQQQ found at
CC the N-terminus of TBP. MAb 1C2 has been shown to have a high affinity
CC for polyglutamine repeats with a proportional affinity to the number
CC of glutamine repeats. This affinity has been used to identify genes
CC encoding proteins containing long polyglutamine repeats which are
CC implicated in neurodegenerative diseases. A screen of an expression
CC library, generated from a lymphoblastic cell line from a patient
CC suffering from spinocerebellar ataxia (SCA), with MAb 1C2 isolated 6 new
CC sequences (AAT78906-T78911) encoding polyglutamine repeats. This
CC sequence is derived from clone DAN15 isolated from a patient suffering
CC from dominant autosomal SCA type 7. MAb 1C2, active fragment of it or
CC nucleic acids encoding it are specifically used to treat Huntington's
CC disease, SCA types 1-5 or 7, X-linked spino-bulbular muscular atrophy
CC (Kennedy disease), dentarorubral-pallidolusial atrophy, dominant
CC autosomal spinocerebellar ataxia, familial spastic paraplegia, bipolar
CC affective disorder, manic depressive psychoses and schizophrenia.
XX
SQ Sequence 54 BP; 21 A; 18 C; 15 G; 0 U; 0 other;

Query Match 64.8%; Score 16.2; DB 18; Length 54;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgag 22
||| |||||||||||| ||
Db 13 cagcagcagcaacagcagcag 33

RESULT 8
AAV17235
ID AAV17235 standard; DNA; 57 BP.
XX
AC AAV17235;
XX
DT 29-JUN-1998 (first entry)
XX
DE SCA2 gene CAG repeat unit fragment.
XX
KW SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9803679-A1.
XX
PD 29-JAN-1998.
XX
PF 18-JUL-1996; 96WO-JP01999.
XX
PR 18-JUL-1996; 96WO-JP01999.
XX
PA (SRLS-) SRL INC.
XX
PI Sanpei K, Tsuji S;
XX
DR WPI; 1998-120796/11.
XX
PT Diagnosing spinocerebellar ataxis type II - by PCR and determining
PT number of CAG repeat units
XX
PS Disclosure; Page 14; 23pp; Japanese.
XX
CC This sequence represents a fragment of the SCA2 gene. It can be used in
CC the method of the invention for diagnosing spinocerebellar ataxis type
CC II, by performing PCR on the test DNA using two primers hybridising to
CC parts of the SCA2 gene sequence, and determining the number of CAG
CC repeats in the amplified products. The method provides an easy means for
CC the diagnosis of spinocerebellar ataxis type II.
XX
SQ Sequence 57 BP; 16 A; 23 C; 18 G; 0 U; 0 other;

Query Match 64.8%; Score 16.2; DB 19; Length 57;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgag 22
||| |||||||||||| ||
Db 10 cagcagcagcaacagcagcag 30

RESULT 9
AAH24422/c
ID AAH24422 standard; DNA; 45 BP.
XX
AC AAH24422;
XX
DT 02-AUG-2001 (first entry)
XX
DE Oligonucleotide encoding eukaryotic consensus signal peptide #1.
XX
KW Eukaryotic; consensus; signal peptide; chlorella; gene expression;
KW protein production; human growth hormone; ds.
XX
OS Unidentified.
XX
PN JP2000354490-A.
XX
PD 26-DEC-2000.
XX
PF 15-JUN-1999; 99JP-0168271.
XX
PR 15-JUN-1999; 99JP-0168271.
XX
PA (TOYT) TOYOTA JIDOSHA KK.
XX
DR WPI; 2001-275809/29.
DR P-PSDB; AAB97091.
XX
PT New signal peptides useful for the preparation of human growth hormone
PT and transformed chlorella -
XX
PS Example 1; Page 4; 15pp; Japanese.
XX
CC The present sequence is provided in a specification relating to signal
CC peptides for expression and secretion of a protein in chlorella. The
CC peptides are of the formula:
CC Met-Ala-Asn-Lys-X_1-(Leu)_n-X_2-Ala-Ser-Gly.
CC X_1 = Ser or Leu;
CC n = an integer of 5-15;
CC X_2 = Gly-Ser-Leu or Pro-Leu-Ala.
CC The signal peptides are useful in the preparation of human growth
CC hormone and transformed chlorella. Signal peptides, DNA encoding the
CC peptides, gene expression cassettes, recombinant vectors containing the
CC cassettes, and transformants having the vectors are provided. The
CC present sequence encodes a signal peptide of the invention.
XX
SQ Sequence 45 BP; 1 A; 18 C; 15 G; 11 T; 0 other;

Query Match 64.0%; Score 16; DB 22; Length 45;
Best Local Similarity 79.2%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 cagtagcagcaacagcatgagacc 25
||| ||||||| ||||| | || |
Db 27 CAGCAGCAGCAGCAGGCGAGC 4

RESULT 10
AAH24423/c
ID AAH24423 standard; DNA; 54 BP.
XX
AC AAH24423;
XX
DT 02-AUG-2001 (first entry)
XX
DE Oligonucleotide encoding eukaryotic consensus signal peptide #2.
XX
KW Eukaryotic; consensus; signal peptide; chlorella; gene expression;
KW protein production; human growth hormone; ds.
XX
OS Unidentified.
XX
PN JP2000354490-A.
XX
PD 26-DEC-2000.
XX
PF 15-JUN-1999; 99JP-0168271.
XX
PR 15-JUN-1999; 99JP-0168271.
XX
PA (TOYT) TOYOTA JIDOSHA KK.
XX
DR WPI; 2001-275809/29.
DR P-PSDB; AAB97092.
XX
PT New signal peptides useful for the preparation of human growth hormone
PT and transformed chlorella -
XX
PS Example 1; Page 4; 15pp; Japanese.
XX
CC The present sequence is provided in a specification relating to signal
CC peptides for expression and secretion of a protein in chlorella. The

```
CC   peptides are of the formula:
CC   Met-Ala-Asn-Lys-X_1-(Leu)_n-X_2-Ala-Ser-Gly.
CC   X_1  = Ser or Leu;
CC   n  = an integer of 5-15;
CC   X_2  = Gly-Ser-Leu or Pro-Leu-Ala.
CC   The signal peptides are useful in the preparation of human growth
CC   hormone and transformed chlorella. Signal peptides, DNA encoding the
CC   peptides, gene expression cassettes, recombinant vectors containing the
CC   cassettes, and transformants having the vectors are provided. The
CC   present sequence encodes a signal peptide of the invention.
XX
SQ   Sequence 54 BP; 1 A; 21 C; 18 G; 14 T; 0 other;


  Query Match             64.0%;  Score 16;  DB 22;  Length 54;
  Best Local Similarity   79.2%;  Pred. No. 9.2e+02;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      2 cagtagcagcaacagcatgagacc 25
          ||| ||||||| ||||| | || |
Db     27 CAGCAGCAGCAGCAGGCGAGC 4


RESULT  11
AAA66287
ID   AAA66287 standard; DNA; 20 BP.
XX
AC   AAA66287;
XX
DT   09-OCT-2000  (first entry)
XX
DE   Dog genomic marker oligonucleotide sequence SEQ ID NO:149.
XX
KW   Dog; genome; genomic marker; radiation hybrid map; identification;
KW   chromosome location; gene marker; polymorphic microsatellite marker;
KW   phenotype; behaviour; pedigree; ss.
XX
OS   Canis familiaris.
XX
PN   WO200029615-A2.
XX
PD   25-MAY-2000.
XX
PF   15-NOV-1999;   99WO-IB01907.
XX
PR   13-NOV-1998;   98US-0108193.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Galibert F,  Andre C;
XX
DR   WPI; 2000-387821/33.
XX
PT   New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT   for e.g. identifying genes implicated in phenotypic and behavioral
PT   traits or in genetic diseases and for studying dog pedigrees  -
XX
PS   Claim 1; Page 59; 87pp; English.
XX
CC   The present invention describes a radiation hybrid map of the dog
CC   (Canine familiaris) genome comprising the genome location of a marker
CC   selected from AAA66139 to AAA66942. The radiation hybrid map is useful
CC   for identifying and localising dog genes, since it covers approximately
CC   80 % of the dog genome and provides a dense map integrating different
CC   types (i.e. Type I and Type II) of markers. The map and the dog genome
CC   markers (or complementary sequences) are especially useful to identify
CC   genes responsible for phenotypic and behavioural traits in dogs, to
CC   identify morbid genes, to analyse diseases and identify implicated genes
CC   in such diseases and their alleles, and to study dog pedigrees. They
CC   may also be useful for isolating corresponding human gene sequences
CC   e.g. genes involved in genetic diseases.
XX
SQ   Sequence 20 BP; 7 A; 6 C; 7 G; 0 U; 0 other;


  Query Match             63.2%;  Score 15.8;  DB 21;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      6 agcagcaacagcatgagac 24
          ||||||| ||||| |||||
Db      2 agcagcagcagcaggagac 20


RESULT  12
AAA04482/c
ID   AAA04482 standard; DNA; 29 BP.
XX
AC   AAA04482;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Polymorphic fragment of hypertension associated gene PGIS.
XX
KW   Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW   Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW   Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
KW   polycystic kidney disease; von Willebrands disease;  forensic; human;
KW   tuberous sclerosis; hereditary hemorrhagica telangiectasia;
KW   familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW   Ehlers-Danlos syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   EP955382-A2.
XX
PD   10-NOV-1999.
XX
PF   07-MAY-1999;   99EP-0250150.
XX
PR   07-MAY-1998;   98US-0084641.
PR   03-MAY-1999;   99US-0304232.
XX
PA   (AFFY-) AFFYMETRIX INC.
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   Fan JB,  Chakravarti A,  Haluska MK;
XX
DR   WPI; 2000-107928/10.
XX
PT   Novel nucleic acids containing polymorphisms used in the diagnosis of
PT   hypertension -
XX
PS   Claim 1; Page 38; 53pp; English.
XX
CC   The invention provides polymorphic fragments of genes associated with
CC   hypertension. The nucleic acids including the polymorphic sites can be
CC   used as probes or primers for expressing variant proteins. Detection of
CC   the polymorphisms is useful in designing prophylactic and therapeutic
CC   regimes customized to underlying abnormalities. The polymorphisms can be
CC   used for association studies for hypertension, and in hypertension
CC   diagnostic assays. Where the polymorphisms have strong correlation with
CC   hypertension, within a gene, they are likely to have a causative role in
CC   hypertension. This information can be used to find the precise role of a
CC   polymorphism in the disease, and this can be used to identify potential
CC   drugs which combat the disease. The polymorphisms can be tested for
CC   association with other diseases e.g. agammaglobulinemia, diabetes
CC   insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC   syndrome, Fabrys disease, familial hypercholesterolemia, polycystic
CC   kidney disease, hereditary spherocytosis, von Willebrands disease,
CC   tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC   colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC   acute intermittent porphyria. The polymorphic forms can also be used in
CC   forensics to identify individuals.
XX
SQ   Sequence 29 BP; 3 A; 9 C; 8 G; 8 T; 1 other;
```

Query Match 63.2%; Score 15.8; DB 21; Length 29;
Best Local Similarity 81.0%; Pred. No. 1e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy       2 cagtagcagcaacagcatgag 22
           |||||||||:|| |||||  ||
Db      23 CAGTAGCARCAGCAGCAACAG 3
```

RESULT 13
AAH48359/c
ID AAH48359 standard; DNA; 38 BP.
XX
AC AAH48359;
XX
DT 21-SEP-2001 (first entry)
XX
DE Human FOAP-9 PCR primer #7.
XX
KW Human; FOAP-9; membrane surface protein; macrophage function;
KW modulator; pulpy arteriosclerosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001136975-A.
XX
PD 22-MAY-2001.
XX
PF 18-NOV-1999; 99JP-0327898.
XX
PR 18-NOV-1999; 99JP-0327898.
XX
PA (TAIS) TAISHO PHARM CO LTD.
XX
DR WPI; 2001-387287/41.
XX
PT New gene and its encoded protein FOAP-9, useful for the diagnosis of
PT pulpy arteriosclerosis -
XX
PS Example 5; Page 7; 15pp; Japanese.
XX
CC The invention relates to human FOAP-9 protein comprising a fully defined
CC sequence of 463 amino acids as given in the specification or a membrane
CC surface protein comprising the defined sequence in which at least one
CC amino acid is deleted, replaced or added. The protein has macrophage
CC function controlling activity and is useful in the diagnosis of pulpy
CC arteriosclerosis. A DNA sequence encoding the protein and having a
CC fully defined sequence of 1392 base pairs, as given in the
CC specification, is also claimed. The present sequence is a primer
CC used in an example illustrating the invention.
XX
SQ Sequence 38 BP; 3 A; 16 C; 9 G; 10 T; 0 other;

Query Match 63.2%; Score 15.8; DB 22; Length 38;
Best Local Similarity 89.5%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2 cagtagcagcaacagcatg 20
           ||| ||||||| |||||||
Db      32 CAGCAGCAGCAGCAGCATG 14
```

RESULT 14
AAC87437/c
ID AAC87437 standard; DNA; 40 BP.
XX
AC AAC87437;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human SEAP alkaline phosphatase PCR primer, SEQ ID NO:29.
XX
KW Ribonucleoprotein complex; RNP; negative-strand RNA; Sendai virus;
KW Paramyxovirus; envelope protein gene deletion; non-antigenic;
KW non-cytotoxic; gene delivery; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200070055-A1.
XX
PD 23-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-JP03194.
XX
PR 18-MAY-1999; 99JP-0200740.
XX
PA (DNAV-) DNAVEC RES INC.
XX
PI Li H, Shu T, Kuma H, Ueda Y, Asakawa M, Hasegawa M, Iida A;
PI Hirata T;
XX
DR WPI; 2001-007499/01.
XX
PT Ribonucleoprotein complex originating in Paramyxovirus incapable of
PT expressing some envelope proteins, for insertion into target cell with
PT avoidance of problems with antigenicity and cytotoxicity, for use e.g.
PT in gene therapy -
XX
PS Example 15; Page 67; 172pp; Japanese.
XX
CC The invention relates to a ribonucleoprotein comprising a Sendai virus
CC (Paramyxovirus) negative-strand single-stranded RNA from which all the
CC envelope protein genes have been deleted, and a protein complexed with
CC the RNA. The invention also relates to a composition for gene insertion
CC comprising the ribonucleoprotein of the invention and a cationic
CC lipid or cationic polymer; and a method for expressing the foreign
CC gene in a cell comprising the insertion of the ribonucleoprotein into the
CC cell. The ribonucleoprotein complex can be used as a gene delivery
CC device for gene therapy, while avoiding problems with antigenicity
CC and cytotoxicity. The present sequence represents a PCR primer used in
CC an exemplification of the invention.
XX
SQ Sequence 40 BP; 1 A; 14 C; 16 G; 9 T; 0 other;

Query Match 63.2%; Score 15.8; DB 22; Length 40;
Best Local Similarity 89.5%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2 cagtagcagcaacagcatg 20
           ||| ||||||| |||||||
Db      28 CAGCAGCAGCAGCAGCATG 10
```

RESULT 15
AAC87489/c
ID AAC87489 standard; DNA; 40 BP.
XX
AC AAC87489;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human SEAP alkaline phosphatase PCR primer, SEQ ID NO:29.
XX
KW Sendai virus vector; Paramyxovirus vector; F protein deletion;
KW envelope protein gene deletion; virion particle production;
KW host cell complementation; gene delivery; gene therapy;
KW cancer; infectious disease; influenza; AIDS; Japanese encephalitis;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200070070-A1.

XX
PD 23-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-JP03195.
XX
PR 18-MAY-1999; 99JP-0200739.
XX
PA (DNAV-) DNAVEC RES INC.
XX
PI Li H, Shu T, Kuma H, Ueda Y, Asakawa M, Hasegawa M, Iida A;
PI Tokitou F, Hirata T, Tokusumi T;
XX
DR WPI; 2001-007501/01.
XX
PT Paramyxovirus vector deficient in an envelope gene for high efficiency
PT transfer of a foreign gene to human cells for gene therapy -
XX
PS Example 15; Page 70; 177pp; Japanese.
XX
CC The invention relates to a Sendai virus (Paramyxovirus) vector
CC comprising a ribonucleoprotein complex consisting of negative-strand
CC single-stranded RNA selected for lack of ability to express one or
CC more envelope proteins (particularly the F protein), and a protein
CC complexed with the RNA. The invention also relates to DNA corresponding
CC to the viral RNA or its complementary chain; and a method for the
CC production of virion particles of the vector, comprising the culture of
CC helper cells which express the protein with which the viral RNA is to be
CC complexed and which have been transformed with cDNA corresponding to the
CC gene(s) which has been deleted from the viral vector genome. The method
CC of the invention provides for Paramyxovirus vectors for use in gene
CC therapy for the prevention and treatment of diseases such as cancer and
CC infectious diseases such as influenza, AIDS and Japanese encephalitis.
CC The vector of the invention allows high efficiency gene delivery. The
CC present sequence represents a PCR primer used in an exemplification of
CC the invention.
XX
SQ Sequence 40 BP; 1 A; 14 C; 16 G; 9 T; 0 other;

Query Match 63.2%; Score 15.8; DB 22; Length 40;
Best Local Similarity 89.5%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      2 cagtagcagcaacagcatg 20
          ||| ||||||| |||||||
Db     28 CAGCAGCAGCAGCAGCATG 10
```

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